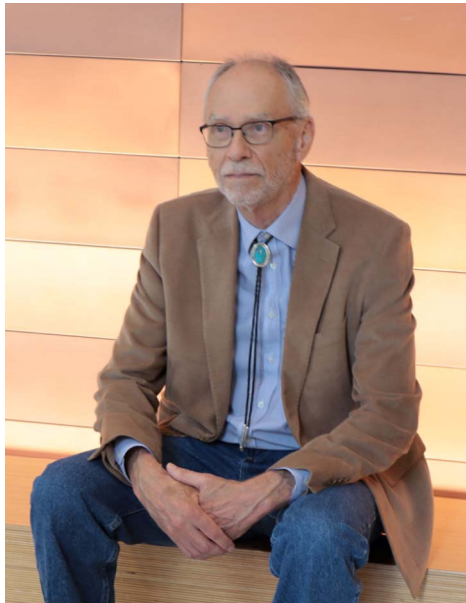


## Special issue on bioinformatics and biophysics in honor of professor Michael Waterman on his 80th birthday



Professor Waterman is one of the founding fathers of computational biology. His research focuses on applying mathematical, statistical, and computer science tools to various biological problems at the molecular level. In addition to the widely used Smith–Waterman algorithm for sequence alignment, Professor Waterman published a landmark paper for DNA mapping with Eric Lander in 1988 and proposed Eulerian-De Bruijn sequence assembly for the next-generation sequencing datasets with Idury in 1995. Professor Waterman is a founding editor of the *Journal of Computational Biology* and a founding member of the Annual International Conference on Research in Computational Molecular Biology (RECOMB), and he also authored one of the earliest textbooks in the field: *Introduction to Computational Biology*.

Professor Waterman’s contribution is well recognized in the scientific community. He holds a variety of honors, including member of the American Academy of Arts and Sciences (1995), the National Academy of Sciences (2001), and the National Academy of Engineering (2012); foreign member

of the French Académie des Sciences (2005) and the Chinese Academy of Sciences (2013). He was also elected fellow of Guggenheim (1995), the American Association for the Advancement of Science (1990), Institute of Mathematical Statistics (1991), Society of Industrial and Applied Mathematics (2009), International Society of Computational Biology (2009) and National Academy of Inventors (2018).

To celebrate Professor Waterman's 80th birthday, *Communications in Information and Systems* (CIS) publishes a special issue on bioinformatics and biophysics in 2022. As branches of computational biology, bioinformatics and biophysics involve the development and application of data-driven approaches, physical and mathematical modelling, and computational simulations to the study of biological systems. The advent of massive biological data and the availability of high-performance computers have paved the way for biological sciences to undertake a historic transition from qualitative to quantitative. However, to attack challenging problems at the forefront of bioinformatics and biophysics, novel mathematical models and efficient computational algorithms are still indispensable. This special issue is called to advance the development of mathematical models and computational algorithms in the fields of bioinformatics and biophysics.

This special issue constitutes six papers, which cover a wide range of topics in bioinformatics and biophysics, such as genomic sequence analysis, mathematical modeling of circadian system, DNA similarity analysis, RNA secondary structure prediction, calculating electrostatic free energy of proteins, and design of mutation-proof COVID-19 monoclonal antibodies.

Finally, we would like to thank the authors for their excellent contributions and patience that make this special issue possible. The time, effort, and valuable work of all anonymous reviewers on these papers are also very greatly acknowledged.

#### **Guest Editorial Board:**

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